

FILE 'MEDLINE' ENTERED AT 14:38:55 ON 06 AUG 2007

L1 178942 S (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)  
L2 810 S L1 AND (VPR OR VIRAL PROTEIN R)  
L3 8 S L2 AND (MONOCLONAL ANTIBOD?)  
L4 83 S L2 AND ANTIBOD?  
L5 75 S L4 NOT L3  
L6 6 S L5 AND ANTI-VPR

FILE 'BIOSIS' ENTERED AT 14:43:34 ON 06 AUG 2007

L7 172040 S (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)  
L8 923 S L7 AND (VPR OR VIRAL PROTEIN R)  
L9 58 S L8 AND ANTIBOD?  
L10 8 S L9 AND MONOCLONAL  
L11 50 S L9 NOT L10

=> log off

# Vpr Ab Epitope Map

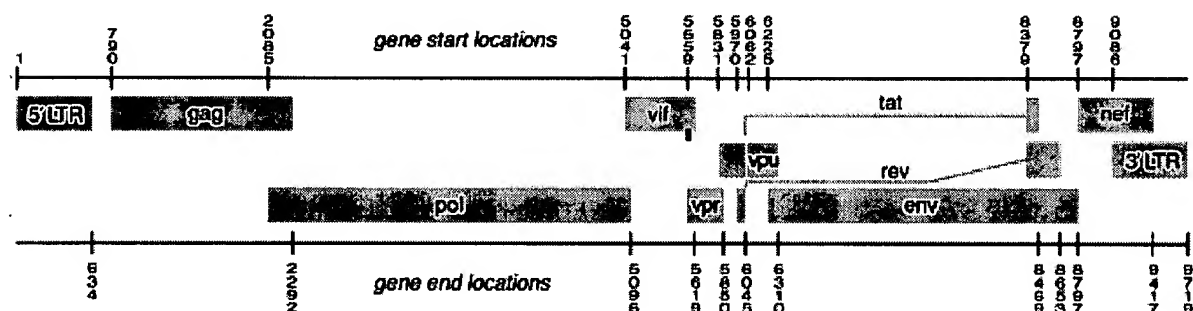
The names of MABs and the location of well characterized linear binding sites of 21 amino acids or less are indicated relative to the protein sequences of the HXB2 clone. This map is meant to provide the relative location of epitopes on a given protein, but the HXB2 sequence may not actually bind to the MAb of interest, as it may vary relative to the sequence for which the epitope was defined. Above each linear binding site, the MAb name is given followed by the species in parentheses. Human is represented by 'h', non-human primate by 'p', mouse by 'm', and others by 'o'. More precise species designations for any given MAb can be found using the web search interface.

```
MEQAPEDQGPQREPHNEWTLLELLEELKNEAVRHFPRIWLHGLGQHIYETY
      |         |         |         |         |         |
      10        20        30        40        50

GDTWAGVEAIIIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS
      |         |         |         |         |
      60        70        80        90
```

Last modified: Wed Apr 11 14:48:25 2007

Query location shown as red bar in map between reading frames 1 and 2.



Query: seq1 EQAPEDQGPQR

Query Length: 11

HXB2 Location: genome: 5562→5594 protein: Vpr 2→12

Alignment used: HIV1VprPRO, 910 sequences

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alignment below in format

table  
fasta  
mase  
pretty

"-" = identity to query sequence

"." = gap in sequence

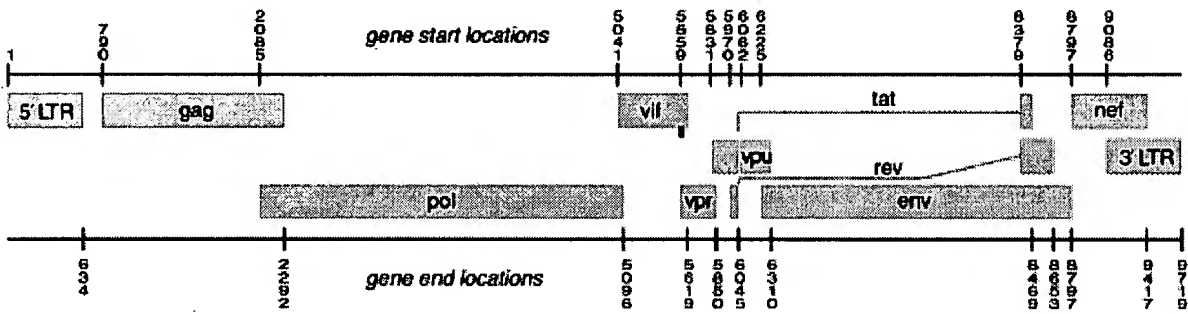
"RED" = perfect identity to query sequence

```

                                seq1 EQAPEDQGPQ R
      B.FR.83.HXB2_K03455 ----- -
    A.SN.01.DDI579_AY521629 ----- -
    A.SN.01.DDJ369_AY521631 ----- -
    A.SN.96.DDJ360_AY521630 ----- -
    A.UA.x.98UA0116_AF413973 ----- -
    A.UA.x.98UA0116_AF413974 ----- -
    A.UA.x.98UA0116_AF413975 ----- -
    A.UA.x.98UA0116_AF413976 ----- -
    A1.KE.00.KER2008_AF457052 ----- -
    A1.KE.00.KER2009_AF457053 ----- -
    A1.KE.00.KER2012_AF457055 ----- -
    A1.KE.00.KNH1144_AF457066 ----- -
    A1.KE.00.KNH1199_AF457067 ----- -
    A1.KE.00.KNH1207_AF457068 -R----- -
  
```

A1.KE.00.KNH1209\_AF457069 ----- -  
A1.KE.00.KNH1211\_AF457070 --T----- -  
A1.KE.00.KNH1214\_AF457071 ----- K  
A1.KE.00.KSM4024\_AF457077 ----- -  
A1.KE.00.KSM4030\_AF457079 -----P -  
A1.KE.00.MSA4069\_AF457080 ----- -  
A1.KE.00.MSA4070\_AF457081 ----- -  
A1.KE.00.MSA4072\_AF457083 ----- -  
A1.KE.00.MSA4076\_AF457084 ----- -  
A1.KE.00.MSA4079\_AF457086 ----- -  
A1.KE.00.NKU3005\_AF457089 ----- -  
A1.KE.00.NKU3007\_AF457091 ----- -  
A1.KE.86.ML013\_10\_AY322184 ----- -

Query location shown as red bar in map between reading frames 1 and 2.



Query: seq1

CEQAPEDQGPQ

Query Length: 11

HXB2 Location: genome: 5559→5591 protein: Vpr 1→11

Alignment used: HIV1VprPRO, 910 sequences

Summarize All

Summarize By Subtype

Find Other Matches

Download

alignment below in format

table	▲
fasta	▢
mase	▢
pretty	▼

"-" = identity to query sequence  
"." = gap in sequence  
"RED" = perfect identity to query sequence

	seq1	CEQAPEDQGP	Q
B.FR.83.HXB2_K03455	M	-----	-
A.SN.01.DDI579_AY521629	M	-----	-
A.SN.01.DDJ369_AY521631	M	-----	-
A.SN.96.DDJ360_AY521630	M	-----	-
A.UA.x.98UA0116_AF413973	M	-----	-
A.UA.x.98UA0116_AF413974	M	-----	-
A.UA.x.98UA0116_AF413975	M	-----	-
A.UA.x.98UA0116_AF413976	M	-----	-
A1.KE.00.KER2008_AF457052	M	-----	-
A1.KE.00.KER2009_AF457053	M	-----	-
A1.KE.00.KER2012_AF457055	M	-----	-
A1.KE.00.KNH1144_AF457066	M	-----	-
A1.KE.00.KNH1199_AF457067	M	-----	-
A1.KE.00.KNH1207_AF457068	M	R-----	-

A1.KE.00.KNH1209\_AF457069 M----- -  
A1.KE.00.KNH1211\_AF457070 M--T----- -  
A1.KE.00.KNH1214\_AF457071 I----- -  
A1.KE.00.KSM4024\_AF457077 M----- -  
A1.KE.00.KSM4030\_AF457079 M----- P  
A1.KE.00.MSA4069\_AF457080 M----- -  
A1.KE.00.MSA4070\_AF457081 M----- -  
A1.KE.00.MSA4072\_AF457083 M----- -  
A1.KE.00.MSA4076\_AF457084 M----- -  
A1.KE.00.MSA4079\_AF457086 M----- -  
A1.KE.00.NKU3005\_AF457089 M----- -  
A1.KE.00.NKU3007\_AF457091 M----- -  
A1.KE.86.ML013\_10\_AY322184 M----- -